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Edited by Ina Körner
Institute of Wastewater Management and Water Protection
Hamburg University of Technology (TUHH)
Hamburg, Germany

With the assistance of
Gerlinde Löbkens, TuTech Innovation GmbH, Hamburg, Germany
Steffen Walk, Institute of Wastewater Management and Water Protection, TUHH

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Christiane Lüdke (11, 41, 80, 155)
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TB-O_06 Determining the mechanisms of nitrous oxide emission under contrasting soil disturbance levels and organic amendments

Grave, R.A. [2]; Mezzari, M.P. [1]; da Silva, M.L.B. [1]; Cassol, P.C. [3]; Nicoloso, R.S.[1]

[1] Embrapa Swine and Poultry, C.Postal 21 Concórdia-SC, Brazil

[2] IFC-Concórdia

[3] UDESC-Lages

rodrigo.nicoloso@embrapa.br

Objectives

Soil management practices can affect soil abiotic factors (e.g., pH, temperature, water saturation, nitrate and labile organic carbon contents) and the abundance of nitrifying and denitrifying bacteria communities regulating N_2O efflux from soils. The objective of this study was to investigate the impact of N sources on N_2O emissions from a Nitisol under contrasting soil disturbance levels.

Methodology

We evaluated short-term N_2O emission from a Rhodic Nitisol under contrasting soil disturbance [undisturbed (US) and disturbed soil (DS)] and N sources [140 kg N ha^{-1} as urea, raw swine slurry (RS), anaerobically digested swine slurry (ADS), composted swine slurry (CS), and a control treatment without N]. N_2O emissions were correlated with soil temperature, water-filled pore space (WFPS), dissolved organic carbon (DOC), ammonium (NH_4^+-N) and nitrate (NO_3^--N) contents, and dominant nitrifying and denitrifying catabolic genes. Real-time quantitative PCR (qPCR) was used to assess specific catabolic nitrifying-ammonium monooxygenase (amoA), and denitrifying nitrate- (narG), nitrite- (nirS), nitric oxide- (norB) and nitrous oxide reductases (nosZ) genes [1,2].

Results

N_2O emissions from US amended with ADS and CS was 47.5 and 16.6% lower than RS (5.6 kg N_2O-N ha^{-1}), respectively. However, no differences in N_2O emissions were observed among the fertilization treatments in DS. Water-filled pore space (WFPS) was consistently higher in the US increasing N_2O emission in comparison to DS. The WFPS effects on N_2O emissions was pronounced above 0.6 cm^3 cm^{-3} ($r=0.565$, $p<0.001$). Increased NO_3^--N contents in DS stimulated N_2O emission ($r=0.667$, $p<0.01$) but had negligible effects in US. The increasing soil NO_3^--N ($r=0.396$ and $p<0.05$) and WFPS (0.391 and $p<0.05$) was accompanied by the increasing abundance of nitrate reductases (*narG*) genes. Nitric oxide reductase (*qnorB*) gene was mostly affected by soil WFPS ($r=0.313$ and $p<0.05$) while the proportion of *narG/nosZ* genes decreased with higher DOC/NO_3^--N ratios ($r=-0.409$, $p<0.01$). N_2O emission had significant correlations with *narG* ($r=0,620$, $p<0.001$), *narG/nosZ* ($r=0.722$, $p<0.001$) and *qnorB/nosZ* ($r=0,603$, $p<0.001$) genes. Soil fertilization increased the abundance of *narG* gene (RS and CS) and the ratio of *narG/nosZ* (UR, RS, and CS) and *qnorB/nosZ* genes (CS) in the soil, enhancing N_2O emissions. Multivariate analysis revealed a higher similarity on the variance of soil N_2O emissions with the abundance and ratios of denitrifying bacteria communities in the US while soil abiotic factors were the major mechanisms that regulated soil N_2O emissions from DS.

Conclusion

Higher soil moisture regime and the application of RS and CS in US increased the *narG/nosZ* and *qnorB/nosZ* ratios and N_2O emissions in relation to DS. N_2O emissions are regulated by a complex interaction between soil abiotic factors and abundance of denitrifying bacteria communities in conservative agroecossystems (US). In oxidative environments such as DS, however, N_2O emissions seem to be mostly regulated by soil abiotic factors.

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